

ENTERED

Serial Number: 09/836,544

RECEIVED
MAR 01 2002
OFFICE OF PETITIONS

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra/invalid headings used by an applicant, specifically: _____
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/836,544

DATE: 12/07/2001
TIME: 19:09:11

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF3\12072001\I836544.raw

3 <110> APPLICANT: The General Hospital Corporation
5 <120> TITLE OF INVENTION: Rapid Immunoselection Cloning Method
7 <130> FILE REFERENCE: 11-88L
9 <140> CURRENT APPLICATION NUMBER: US 09/836,544
10 <141> CURRENT FILING DATE: 2001-04-17
12 <150> PRIOR APPLICATION NUMBER: US 07/983,647
13 <151> PRIOR FILING DATE: 1992-12-01
15 <150> PRIOR APPLICATION NUMBER: US 07/553,759
16 <151> PRIOR FILING DATE: 1990-07-13
18 <150> PRIOR APPLICATION NUMBER: US 07/498,809
19 <151> PRIOR FILING DATE: 1990-03-23
21 <150> PRIOR APPLICATION NUMBER: US 07/379,076
22 <151> PRIOR FILING DATE: 1989-07-13
24 <150> PRIOR APPLICATION NUMBER: US 07/160,416
25 <151> PRIOR FILING DATE: 1988-02-25
27 <160> NUMBER OF SEQ ID NOS: 37
29 <170> SOFTWARE: PatentIn Ver. 2.0
31 <210> SEQ ID NO: 1
32 <211> LENGTH: 2932
33 <212> TYPE: DNA
34 <213> ORGANISM: Artificial Sequence
36 <220> FEATURE:
37 <223> OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
38 sequence of expression vector, pIH3
40 <400> SEQUENCE: 1
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43 gatcaagagc taccaactct ttttccgaag gaactggctt cagcagagcg cagataccaa 120
45 atactgtcct tctagtgtag ccgtagttag gccaccactt caagaactct gtagcaccgc 180
47 ctacatacct cgctctgcta atcctgtttac cagtggctgc tgccagtggc gataagtcgt 240
49 gtcttaccgg gttggactca agacgatagt taccggataa ggcgcagcgg tggggctgaa 300
51 cgggggggttc gtgcacacag cccagcttg ggcgaacgac ctacaccgaa ctgagatacc 360
53 tacagcgtga gctatgagaa agcgcacgc ttcccgaagg gagaaaggcg gacagggtatc 420
55 cggtaagcgg cagggctcga acaggagagc gcacgaggga gcttccaggg ggaaacgcct 480
57 ggtatcttta tagtctgtc ggggtttgcc acctctgact tgagcgtcga tttttgtgat 540
59 gctcgtcagg ggggcggagc ctatggaaaa acgccagcaa cgccgaatta ccgcggtggt 600
61 totcaacgta acactttaca gcggcgcgctc atttgatatg atgcgccccg cttcccagata 660
63 agggagcagg ccagtaaaaag cattaccctg ggtgggggttc ccgagcggcc aaaggaggca 720
65 gactctaaat ctgccgtcat cgaacttcgaa ggttcgaatc cttccccac caccatcact 780
67 ttcaaaagtc cgaaagaatc tgctccctgc ttgtgtgttg gaggtcgtg agtagtgcgc 840
69 gagtaaaatt taagctacaa caaggcaagg cttgaccgac aattgcatga agaactcgtc 900
71 taggggttagg cgttttgcgc tgcttcgcaat tgtagcggcc agatatacgc gttgacattg 960
73 attattgact agttattaat agtaataat tacgggtc ttagttcata gcccatatat 1020
75 ggagttccgc gttacataac ttacggtaaa tggcccgctt ggctgaccgc ccaacgaccc 1080
77 ccgcccattg acgtcaataa tgacgtatgt tcccatagta acgccaatag ggactttcca 1140
79 ttgacgtcaa tgggtggact atttacggta aactgcccac ttggcagtac atcaagtgt 1200
81 tcatatgcca agtacgcccc ctattgacgt caatgacggt aaatggcccc cctggcatta 1260
83 tgcccagtac atgaccttat gggactttcc tacttggcag tacatctacg tattagtcat 1320

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87 ctcacgggga tttccaagtc tccaccccat tgacgtcaat gggagtttgt tttggacca 1440
89 aaatcaacgg gactttccaa aatgtcgtaa caactccgcc ccattgacgc aaatgggcgg 1500
91 aattcctggg cgggactggg gaggggcgag ccctcagatg ctgcatataa gcagctgctt 1560
93 tttgcctgta ctgggtctct ctggttagac cagatctgag cctgggagct ctctggctaa 1620
95 ctagagaacc cactgcttaa gcctcaataa agcttctaga gatccctcga cctcgaggga 1680
97 tcttccatac ctaccagttc tgcgcctgca ggtcgcggcc gcgactctag aggatctttg 1740
99 tgaaggaacc ttacttctgt ggtgtgacat aattggacaa actacctaca gagatttaaa 1800
101 gctctaaggt aaatataaaa tttttaagtg tataatgtgt taaactactg attctaattg 1860
103 tttgtgtatt ttagattcca acctatggaa ctgatgaatg ggagcagtg tggaatgcct 1920
105 ttaatgagga aaacctgttt tgctcagaag aaatgccatc tagtgatgat gaggctactg 1980
107 ctgactctca acattctact cctccaaaaa agaagagaaa ggtagaagac cccaaggact 2040
109 ttocctcaga attgctaagt tttttgagtc atgctgtgtt tagtaataga actcttgctt 2100
111 gctttgctat ttacaccaca aaggaaaaag ctgcaactgt atacaagaaa attatggaaa 2160
113 aatattctgt aacctttata agtaggcata acagttataa tcataacata ctgttttttc 2220
115 ttactccaca caggcataga gtgtctgcta ttaataacta tgctcaaaaa ttgtgtacct 2280
117 ttagctttttt aatttgtaaa ggggttaata aggaatatat gatgtatagt gccttgacta 2340
119 gagatcataa tcagccatac cacatttgta gagggtttac ttgctttaaa aaacctccca 2400
121 cacctccccc tgaacctgaa acataaaaatg aatgcaattg ttgttgtaaa cttgtttatt 2460
123 gcagcttata atggttacaa ataaagcaat agcatcacia atttcacaaa taaagcattt 2520
125 ttttcaactgc attctagttg tggtttgctc aaactcatca atgtatctta tcatgtctgg 2580
127 atcctgtgga atgtgtgtca gttagggtgt ggaaagtccc caggctcccc agcaggcaga 2640
129 agtatgcaaa gcatgcatct caattagtca gcaaccagggt gtggaaagtc cccaggctcc 2700
131 ccagcaggca gaagtatgca aagcatgcat ctcaattagt cagcaaccat agtcccgcgc 2760
133 ctaactccgc ccatcccgcc cctaactccg cccagttccg cccattctcc gccccatggc 2820
135 tgactaattt tttttattta tgcagaggcc gaggccgcct cggcctctga gctattccag 2880
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140 <210> SEQ ID NO: 2

141 <211> LENGTH: 1504

142 <212> TYPE: DNA

143 <213> ORGANISM: Homo sapiens

145 <220> FEATURE:

146 <221> NAME/KEY: CDS

147 <222> LOCATION: (7)..(1059)

149 <400> SEQUENCE: 2

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152 1 5 10
154 ttc aat gtt tct tcc aaa ggt gca gtc tcc aaa gag att acg aat gcc 96
155 Phe Asn Val Ser Ser Lys Gly Ala Val Ser Lys Glu Ile Thr Asn Ala
156 15 20 25 30
158 ttg gaa acc tgg ggt gcc ttg ggt cag gac atc aac ttg gac att cct 144
159 Leu Glu Thr Trp Gly Ala Leu Gly Gln Asp Ile Asn Leu Asp Ile Pro
160 35 40 45
162 agt ttt caa atg agt gat gat att gac gat ata aaa tgg gaa aaa act 192
163 Ser Phe Gln Met Ser Asp Asp Ile Asp Asp Ile Lys Trp Glu Lys Thr
164 50 55 60
166 tca gac aag aaa aag att gca caa ttc aga aaa gag aaa gag act ttc 240
167 Ser Asp Lys Lys Lys Ile Ala Gln Phe Arg Lys Glu Lys Glu Thr Phe

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171 Lys Glu Lys Asp Thr Tyr Lys Leu Phe Lys Asn Gly Thr Leu Lys Ile
172          80          85          90
174 aag cat ctg aag acc gat gat cag gat atc tac aag gta tca ata tat 336
175 Lys His Leu Lys Thr Asp Asp Gln Asp Ile Tyr Lys Val Ser Ile Tyr
176 95          100          105          110
178 gat aca aaa gga aaa aat gtg ttg gaa aaa ata ttt gat ttg aag att 384
179 Asp Thr Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Asp Leu Lys Ile
180          115          120          125
182 caa gag agg gtc tca aaa cca aag atc tcc tgg act tgt atc aac aca 432
183 Gln Glu Arg Val Ser Lys Pro Lys Ile Ser Trp Thr Cys Ile Asn Thr
184          130          135          140
186 acc ctg acc tgt gag gta atg aat gga act gac ccc gaa tta aac ctg 480
187 Thr Leu Thr Cys Glu Val Met Asn Gly Thr Asp Pro Glu Leu Asn Leu
188          145          150          155
190 tat caa gat ggg aaa cat cta aaa ctt tct cag agg gtc atc aca cac 528
191 Tyr Gln Asp Gly Lys His Leu Lys Leu Ser Gln Arg Val Ile Thr His
192          160          165          170
194 aag tgg acc acc agc ctg agt gca aaa ttc aag tgc aca gca ggg aac 576
195 Lys Trp Thr Thr Ser Leu Ser Ala Lys Phe Lys Cys Thr Ala Gly Asn
196 175          180          185          190
198 aaa gtc agc aag gaa tcc agt gtc gag cct gtc agc tgt cca gag aaa 624
199 Lys Val Ser Lys Glu Ser Ser Val Glu Pro Val Ser Cys Pro Glu Lys
200          195          200          205
202 ggt ctg gac atc tat ctc atc att ggc ata tgt gga gga ggc agc ctc 672
203 Gly Leu Asp Ile Tyr Leu Ile Ile Gly Ile Cys Gly Gly Gly Ser Leu
204          210          215          220
206 ttg atg gtc ttt gtg gca ctg ctc gtt ttc tat atc acc aaa agg aaa 720
207 Leu Met Val Phe Val Ala Leu Leu Val Phe Tyr Ile Thr Lys Arg Lys
208          225          230          235
210 aaa cag agg agt cgg aga aat gat gag gag ctg gag aca aga gcc cac 768
211 Lys Gln Arg Ser Arg Arg Asn Asp Glu Glu Leu Glu Thr Arg Ala His
212          240          245          250
214 aga gta gct act gaa gaa agg ggc cgg aag ccc cac caa att cca gct 816
215 Arg Val Ala Thr Glu Glu Arg Gly Arg Lys Pro His Gln Ile Pro Ala
216 255          260          265          270
218 tca acc cct cag aat cca gca act tcc caa cat cct cct cca cca cct 864
219 Ser Thr Pro Gln Asn Pro Ala Thr Ser Gln His Pro Pro Pro Pro Pro
220          275          280          285
222 ggt cat cgt tcc cag gca cct agt cat cgt ccc ccg cct cct gga cac 912
223 Gly His Arg Ser Gln Ala Pro Ser His Arg Pro Pro Pro Pro Gly His
224          290          295          300
226 cgt gtt cag cac cag cct cag aag agg cct cct gct ccg tcg ggc aca 960
227 Arg Val Gln His Gln Pro Gln Lys Arg Pro Pro Ala Pro Ser Gly Thr
228          305          310          315
230 caa gtt cac cag cag aaa ggc ccg ccc ctc ccc aga cct cga gtt cag 1008
231 Gln Val His Gln Gln Lys Gly Pro Pro Leu Pro Arg Pro Arg Val Gln
232          320          325          330

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234 cca aaa cct ccc cat ggg gca gca gaa aac tca ttg tcc cct tcc tct 1056
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236 335 340 345 350
238 aat taaaaaagat agaaactgtc tttttcaata aaaagcactg tggatttctg 1109
239 Asn
241 ccctcctgat gtgcatatcc gtacttccat gaggtgtttt ctgtgtgcag aacattgtca 1169
243 cctcctgagg ctgtgggcca cagccacctc tgcattctcg aactcagcca tgtggtcaac 1229
245 atctggagtt tttgtctcc tcagagagct ccatcacacc agtaaggaga agcaatataa 1289
247 gtgtgattgc aagaatggta gaggaccgag cacagaaatc ttagagattt cttgtcccct 1349
249 ctcaggatcat gtgtagatgc gataaatcaa gtgattgggtg tgcctgggtc tcactacaag 1409
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257 <211> LENGTH: 351
258 <212> TYPE: PRT
259 <213> ORGANISM: Homo sapiens
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266 20 25 30
268 Thr Trp Gly Ala Leu Gly Gln Asp Ile Asn Leu Asp Ile Pro Ser Phe
269 35 40 45
271 Gln Met Ser Asp Asp Ile Asp Asp Ile Lys Trp Glu Lys Thr Ser Asp
272 50 55 60
274 Lys Lys Lys Ile Ala Gln Phe Arg Lys Glu Lys Glu Thr Phe Lys Glu
275 65 70 75 80
277 Lys Asp Thr Tyr Lys Leu Phe Lys Asn Gly Thr Leu Lys Ile Lys His
278 85 90 95
280 Leu Lys Thr Asp Asp Gln Asp Ile Tyr Lys Val Ser Ile Tyr Asp Thr
281 100 105 110
283 Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Asp Leu Lys Ile Gln Glu
284 115 120 125
286 Arg Val Ser Lys Pro Lys Ile Ser Trp Thr Cys Ile Asn Thr Thr Leu
287 130 135 140
289 Thr Cys Glu Val Met Asn Gly Thr Asp Pro Glu Leu Asn Leu Tyr Gln
290 145 150 155 160
292 Asp Gly Lys His Leu Lys Leu Ser Gln Arg Val Ile Thr His Lys Trp
293 165 170 175
295 Thr Thr Ser Leu Ser Ala Lys Phe Lys Cys Thr Ala Gly Asn Lys Val
296 180 185 190
298 Ser Lys Glu Ser Ser Val Glu Pro Val Ser Cys Pro Glu Lys Gly Leu
299 195 200 205
301 Asp Ile Tyr Leu Ile Ile Gly Ile Cys Gly Gly Gly Ser Leu Leu Met
302 210 215 220
304 Val Phe Val Ala Leu Leu Val Phe Tyr Ile Thr Lys Arg Lys Lys Gln
305 225 230 235 240
307 Arg Ser Arg Arg Asn Asp Glu Glu Leu Glu Thr Arg Ala His Arg Val
308 245 250 255

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310 Ala Thr Glu Glu Arg Gly Arg Lys Pro His Gln Ile Pro Ala Ser Thr
311                260                265                270
313 Pro Gln Asn Pro Ala Thr Ser Gln His Pro Pro Pro Pro Pro Gly His
314                275                280                285
316 Arg Ser Gln Ala Pro Ser His Arg Pro Pro Pro Pro Gly His Arg Val
317                290                295                300
319 Gln His Gln Pro Gln Lys Arg Pro Pro Ala Pro Ser Gly Thr Gln Val
320 305                310                315                320
322 His Gln Gln Lys Gly Pro Pro Leu Pro Arg Pro Arg Val Gln Pro Lys
323                325                330                335
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326                340                345                350
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330 <211> LENGTH: 874
331 <212> TYPE: DNA
332 <213> ORGANISM: Homo sapiens
334 <220> FEATURE:
335 <221> NAME/KEY: CDS
336 <222> LOCATION: (13)..(723)
338 <400> SEQUENCE: 4
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341                1                5                10
343 ctc agc gtg gtc tgc ctg ctg cac tgc ttt ggt ttc atc agc tgt ttt 99
344 Leu Ser Val Val Cys Leu His Cys Phe Gly Phe Ile Ser Cys Phe
345 15                20                25
347 tcc caa caa ata tat ggt gtt gtg tat ggg aat gta act ttc cat gta 147
348 Ser Gln Gln Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val
349 30                35                40                45
351 cca agc aat gtg cct tta aaa gag gtc cta tgg aaa aaa caa aag gat 195
352 Pro Ser Asn Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp
353                50                55                60
355 aaa gtt gca gaa ctg gaa aat tct gaa ttc aga gct ttc tca tct ttt 243
356 Lys Val Ala Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe
357                65                70                75
359 aaa aat agg gtt tat tta gac act gtg tca ggt agc ctc act atc tac 291
360 Lys Asn Arg Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr
361                80                85                90
363 aac tta aca tca tca gat gaa gat gag tat gaa atg gaa tcg cca aat 339
364 Asn Leu Thr Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn
365                95                100                105
367 att act gat acc atg aag ttc ttt ctt tat gtg ctt gag tct ctt cca 387
368 Ile Thr Asp Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro
369 110                115                120                125
371 tct ccc aca cta act tgt gca ttg act aat gga agc att gaa gtc caa 435
372 Ser Pro Thr Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln
373                130                135                140
375 tgc atg ata cca gag cat tac aac agc cat cga gga ctt ata atg tac 483
376 Cys Met Ile Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr

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VERIFICATION SUMMARY

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